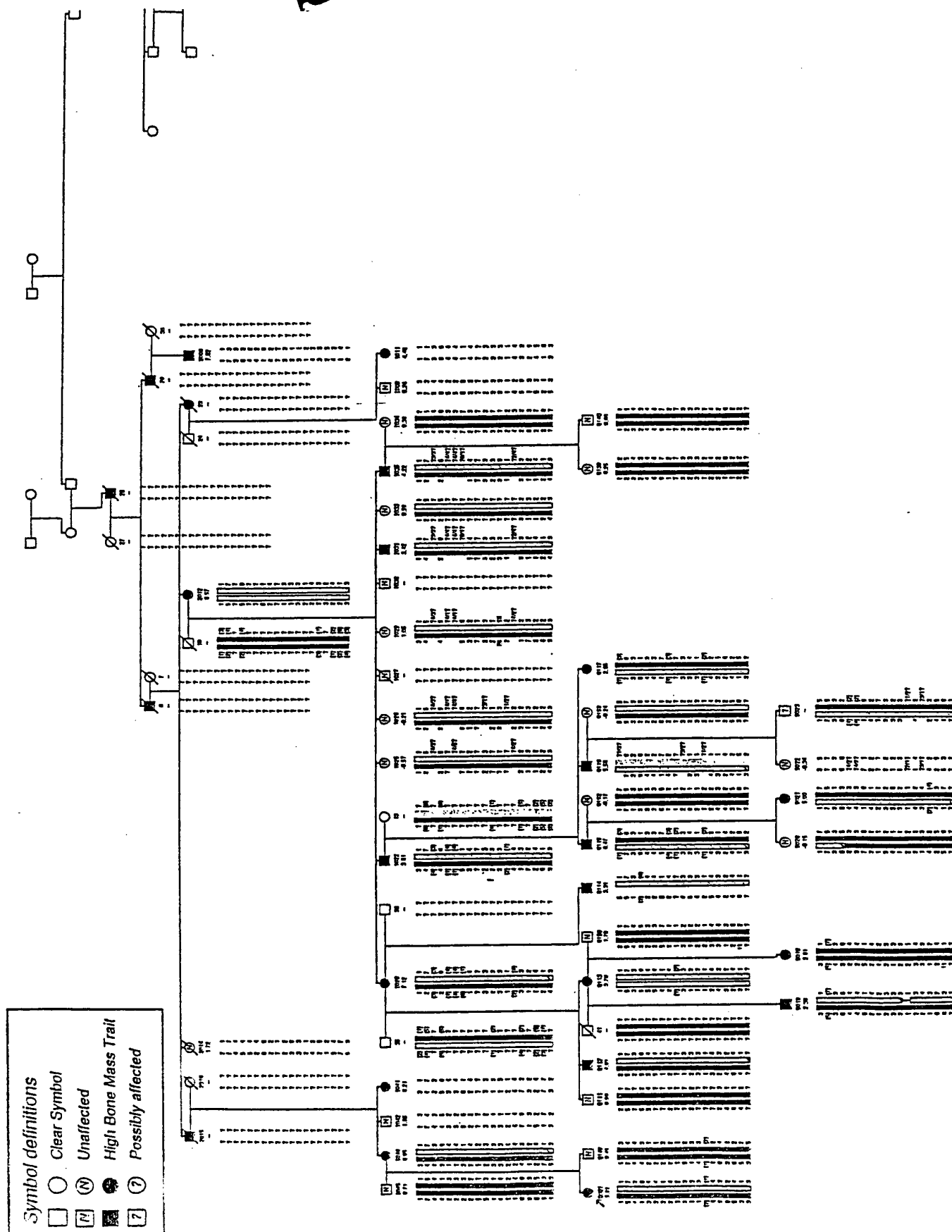
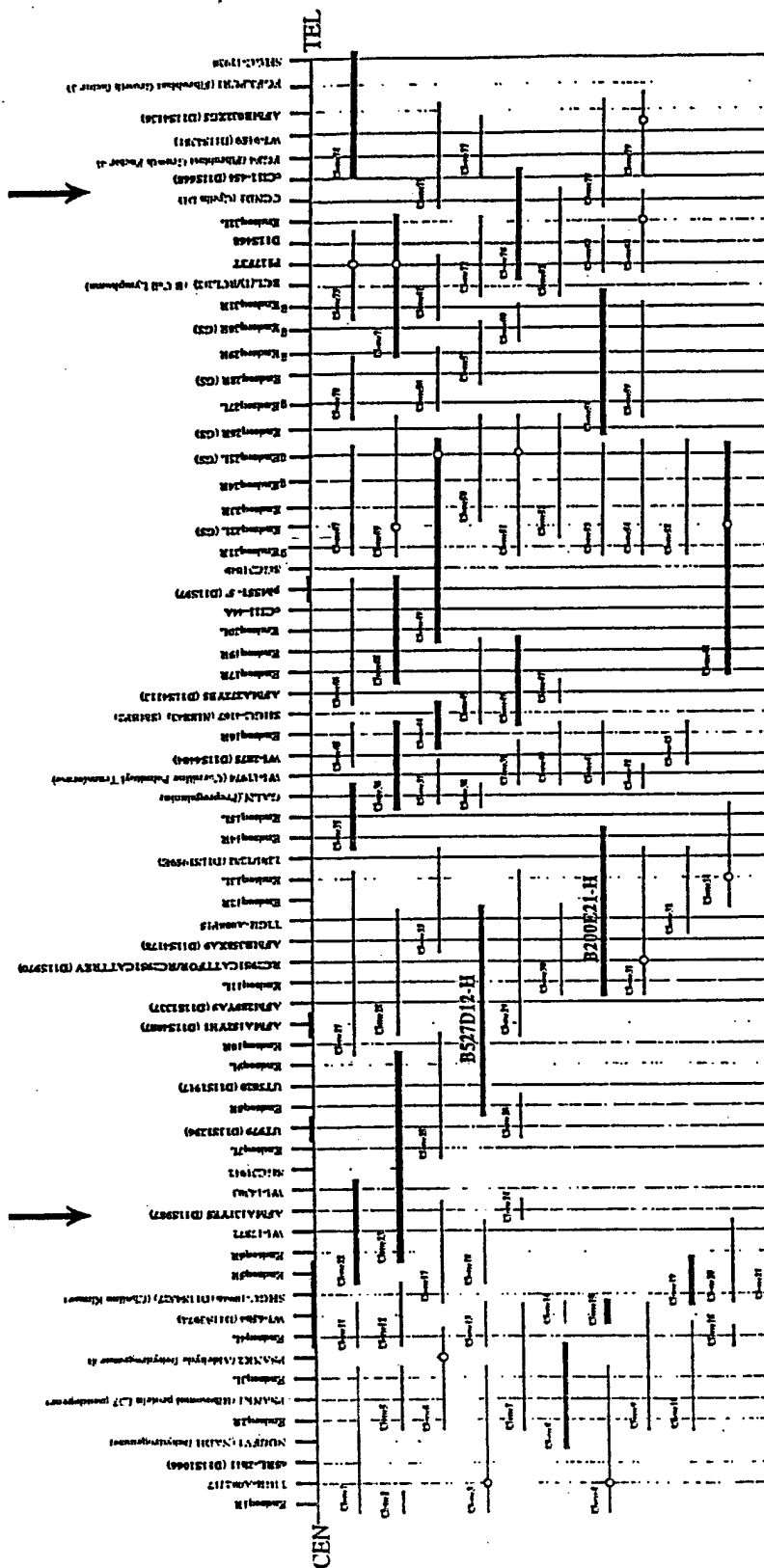


Figure 1.
HBM haplotype indicated with crosshatch



BAC/STS Map of the HBM Region

EST/Gene
Anonymous STS
STSs from BAC Ends
Genetic Marker



— BAC - HTS Complete
- - - Homology on other chromosomes
| Genetic Marker

Exon 1

ACTAAAGCGCCGCCGCCGCCATGGAGCCCGAGTGAGCGCGGGCCGG
GCCCGTCCGGGCCGCCGACAACATGGAGGCAGCGCCGCCCGGGCCGCC
GTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGCTGC
CCGGCCCCCGCCGCCGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549

gccccacagCCTCGCCGCTCCTGCTATTTGCCAACC GCCGGGACGTACGGCTG
GTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCC
TGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTA
CTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAG
ACGGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG
ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTC
AGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAG
GTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGCCTTGGACC
CCGCTCACGGgtaaaccctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945

ccccgtcacagGTACATGTACTGGACAGACTGGGGGTGAGACGCCCCGGATTGA
GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGAC
ATTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCT
ACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGG
CTCGTTCCGgtaggtaccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850

tccctgactgcagGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCC
TGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTC
CATCCATGCCTGCAACAAGCGCACTGGGGGGGAAGAGGAAGGAGATCCTG
AGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGC
AGCCTTTCTgtgagtgccgg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088

tttctcagTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCACCTGT
GCCTGCTGTCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGG
TGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggtgggacg

FIGURE 3A

... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100

ctccacagGAGCCGAGGAGGTGCTGCTGCTGGCCCCGGCGGACGGACCTACGG
AGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGG
ACGACATCCGGCAGCCATTGCCATCGACTACGACCCGCTAGAGGGCTA
TGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTG
GACGGGTCTGGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCG
ATGGCATCGCGGTGCGACTGGGTGGCCCCGAAACCTCTACTGGACCGACAC
GGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAG
ATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACC
CCGTGATGGGgtaagacgggc

..... 3211 nt

Exon 7 Coordinates: 527d12_Contig309G 11311-11482

ttcttctccagCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGT
GTGCCAACTTGGATGGGCAGGAGCGGGCGTGTGCTGGTCAATGCCTCCCT
CGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTAC
TGGGGAGACGCCAAGACAGACAAGATCGAGgtgaggctcctgtgg

..... 13445 nt

Exon 8 Coordinates: 527d12_Contig309G 24927-25143

ccgtcctgcagGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAG
GACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTA
CTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGACAAAGGTCAAG
GCCAGCCGGGACGTCATCATTGACCAGCTGCCCCGACCTGATGGGGCTCA
AAGCTGTGAATGTGGCCAAGGTCGTCGgtgagtcgggggggtc

....2826 nt

Exon 9 Coordinates: 527d12_Contig309G 27969-28256

gttcgcttcagGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACC
TGTGCTTCTTCACACCCACGCAACCCGGTGTGGCTGCCCCATCGGCCT
GGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTG
GTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATA
ACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCT
GGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGA
AGgtagcgtgggc

.....3102.....

FIGURE 3B

005250 006250

Exon 10 Coordinates: 527d12_Contig309G 31358-31582

cctgtgccagACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCAC
GTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA
TGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGT
GGCGCGGCTGGACGGGCAAGTCCGGCAAGTCCTCGTGTGGAGGGACTTG
GACAACCCGAGGTGCTGGCCCTGGATCCCACCAAGGGgtaagtgttgctgtc

.....1297 nt.....

Exon 11 Coordinates: 527d12_Contig309G 32879-33064

gtgcctccagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTG
CGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGG
GCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTACTG
GACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGgtgagggcc
gggct

.....2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454

gtgtcatgcagGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGT
TCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTG
CACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCCTCA
TCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTCCTCC
CGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGC
AGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACA
CTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCgtaagtgcctcatggt

.....2006 nt.....

Exon 13 Coordinates: 527d12_Contig309G 37460-37659

gcctcctctaCGCCCACCACCTTCTTGCTGTTAGCCAGAAATCTGCCATCAGT
CGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCTGCG
ATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTT
CATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGAC
GGGACCCAGgcaggtgccctgtgg

.....6965 nt.....

FIGURE 3C

Exon 14 Coordinates: 527d12_Contig309G 44624-44832

ctttgtcttacagCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACA
GGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTG
GACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAA
GCCATGGGGGTGGTGTCTGCGTGGGGACCGCGACAAGCCCAGGGCCATC
GTCGTCAACGCGGAGCGAGGgtaggaggccaac

.....1404 nt.....

Exon 15 Coordinates: 527d12_Contig309G 46236-46427

ccaccctccgcagGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGA
TCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCAC
CGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAG
CTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGT
CAGgtacgcgcgcgcg

.....686 nt.....

Exon 16 Coordinates: 527d12_Contig309G 47113-47322

ggctgcttcagGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGC
CTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCA
GCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACT
CGCATCCAGGGCCGTGTGCCCCACCTCACTGGCATCCATGCAGTGGAGG
AAGTCAGCCTGGAGGAGTTCTgtacgtgggggc

.....3884 nt.....

Exon 17 Coordinates: 527d12_Contig309G 51206-51331

ttgtctttgcagCAGCCCACCCATGTGCCCCGTGACAATGGTGGCTGCTCCCACAT
CTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCAC
CTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGgtaggtgtgacctaggtgc

....3905 nt.....

Exon 18 Coordinates: 527d12_Contig309G 55236-55472

gttctcctctgtcctccccagAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGC
CACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTT
CCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCG
CCGCCCAGTTCCCCTGCGCGCGGGGTCAAGTGTGTGGACCTGCGCCTGCG
CTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGT
GACGgtgaggccctcc

.....3052 nt.....

FIGURE 3D

0057000105500

Exon 19 Coordinates: 527d12_Contig309G 58524-53634

tctccttgccagCCATCTGCCTGCCCAACCAAGTTCCGGTGTGCGAGCGGCCAGTG
TGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCT
CCGACGAGCTCATGTGTGgtgagccagctt

.....1448 nt.....

Exon 20 Coordinates: 527d12_Contig309G 60082-60319

gtttgtctctggcagAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCCCACAGC
AGTGCCATCGGGCCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGG
TGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGG
GCCAACGGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGC
CCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCCTTCACAGgta
aggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552

cttccttgccagGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGA
TGGGGGGCGGGGGCGGGGTGCCCCCTCTACGACCGGAACCACGTACAG
GGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCC
Ggtgaggggagggg

.....6513 nt.....

Exon 22 Coordinates: 527d12_Contig309G 68065-68162

ttggctctcctcagATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG
TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACC
GTACAGgtaggacatcccctgcag

.....2273 nt.....

FIGURE 3E

00578900-00684560

Exon 23 Coordinates: 527d12_Contig309G 70435-70901

tcaaacattcgggccactgcgagaccgtacagGCCCTACATCATTGAGGAATGGCGCCCCC
GACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGC
CGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACC
CCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGA
CAGCTGCCCCGCCCTCGCCCCGCCACCGAGAGGAGCTACTTCCATCTCTTC
CCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCA
CTCTGGCTTCTCTGTGCCCCCTGTAAATAGTTTTAAATATGAACAAAGAAAAA
ATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGA
AATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAG
AAATATTTATAAACTTAATTTTGTAACA

FIGURE 3F

005250-005250

Figure 4

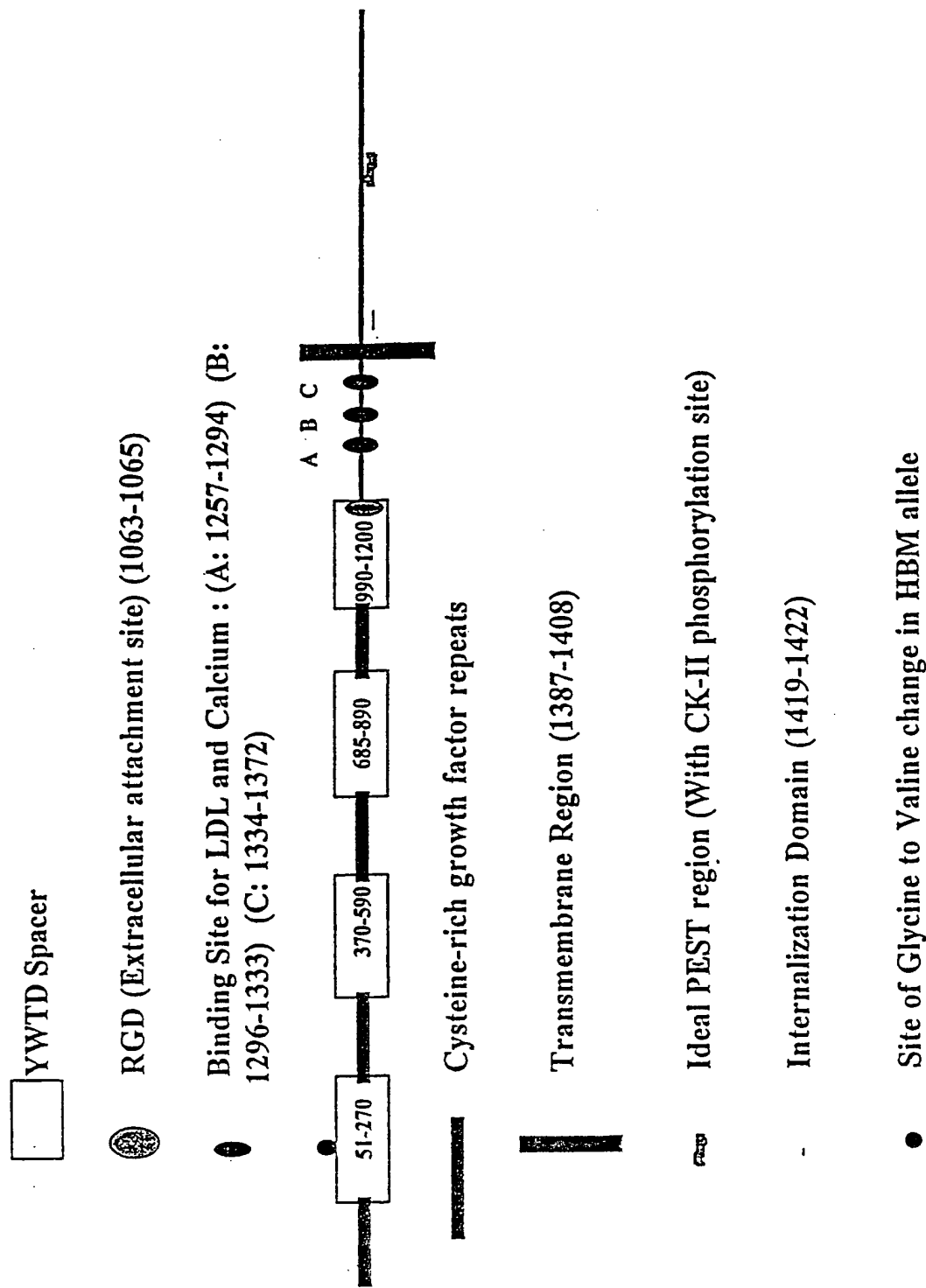
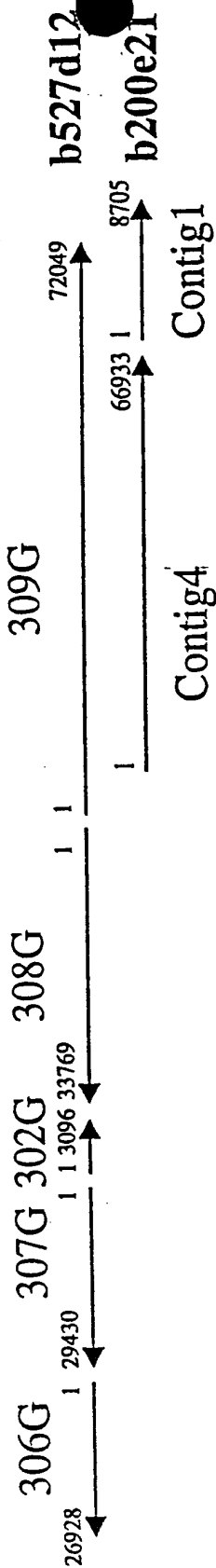
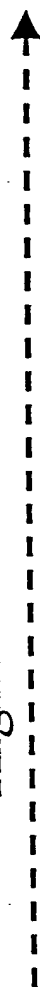
Model for a LDL Receptor-Related protein, Zmax1

Figure 5

High Bone Mass Gene



1	ACTAAAGCGCCGCGCCGCGCCATGEAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC	60
61	GCCGGACAACATGGAGGCAGCGCCGCGCGGGCCCGCTGGCCGCTGCTGCTGCTGCTGCT	120
1	M E A A P P G P P W P L L L L L L	17
121	GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCGCGGCTCGCCGCTCCTGCTATT	180
18	L L L A L C G C P A P A A A S P L L L F	37
181	TGCCAACC GCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT	240
38	A N R R D V R L V D A G G V K L E S T I	57
241	CGTGGTCAGCGGCCTGGAGGATGCGGCCGAGTGGACTTCCAGTTTTC AAGGGAGCCGT	300
58	V V S G L E D A A A V D F Q F S K G A V	77
301	GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC	360
78	Y W T D V S E E A I K Q T Y L N Q T G A	97
361	CGCCGTGCAGAACGTGGTTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG	420
98	A V Q N V V I S G L V S P D G L A C D W	117
421	GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT	480
118	V G K K L Y W T D S E T N R I E V A N L	137
481	CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC	540
138	N G T S R K V L F W Q D L D Q P R A I A	157
541	CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA	600
158	L D P A H G Y M Y W T D W G E T P R I E	177
601	GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC	660
178	R A G M D G S T R K I I V D S D I Y W P	197
661	CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG	720
198	N G L T I D L E E Q K L Y W A D A K L S	217
721	CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT	780
218	F I H R A N L D G S F R Q K V V E G S L	237
781	GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC	840
238	T H P F A L T L S G D T L Y W T D W Q T	257
841	CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC	900
258	R S I H A C N K R T G G K R K E I L S A	277
901	CCTCTACTCACCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC	960
278	L Y S P M D I Q V L S Q E R Q P F F H T	297
961	TCGCTGTGAGGAGGACAATGGCGGCTGCTCCACCTGTGCCTGCTGTCCCCAAGCGAGCC	1020
298	R C E E D N G G C S H L C L L S P S E P	317
1021	TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA	1080
318	F Y T C A C P T G V Q L Q D N G R T C K	337
1081	GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCCGGCGGACGGACCTACGGAGGATCTCGCT	1140
338	A G A E E V L L L A R R T D L R R I S L	357

Figure 6A

1141	GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCAGCCATTGC	1200
358	D T P D F T D I V L Q V D D I R H A I A	377
1201	CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT	1250
378	I D Y D P L E G Y V Y W T D D E V R A I	397
1261	CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA	1320
398	R R A Y L D G S G A Q T L V N T E I N D	417
1321	CCCCGATGGCATCGCGGTGCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC	1380
418	P D G I A V D W V A R N L Y W T D T G T	437
1381	GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTGCGGAGGA	1440
438	D R I E V T R L N G T S R K I L V S E D	457
1441	CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA	1500
458	L D E P R A I A L H P V M G L M Y W T D	477
1501	CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGATGGGCAGGAGCGGCGTGTGCT	1560
478	W G E N P K I E C A N L D G Q E R R V L	497
1561	GGTCAATGCCTCCCTCGGGTGGCCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT	1620
498	V N A S L G W P N G L A L D L Q E G K L	517
1621	CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG	1680
518	Y W G D A K T D K I E V I N V D G T K R	537
1681	GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTTCACGCTGCTGGGGGACTT	1740
538	R T L L E D K L P H I F G F T L L G D F	557
1741	CATCTACTGGACTGACTGGCAGCGCCGAGCATCGAGCGGTGCACAAGGTCAAGGCCAG	1800
558	I Y W T D W Q R R S I E R V H K V K A S	577
1801	CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC	1860
578	R D V I I D Q L P D L M G L K A V N V A	597
1861	CAAGGTGCTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGTGCAGCCACCTGTGCTT	1920
598	K V V G T N P C A D R N G G C S H L C F	617
1921	CTTCACACCCACGCAACCCGGTGTGGCTGCCCATCGGCCTGGAGCTGCTGAGTGACAT	1980
618	F T P H A T R C G C P I G L E L L S D M	637
1981	GAAGACCTGCATCGTGCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG	2040
638	K T C I V P E A F L V F T S R A A I H R	657
2041	GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC	2100
658	I S L E T N N N D V A I P L T G V K E A	677
2101	CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA	2160
678	S A L D F D V S N N H I Y W T D V S L K	697
2161	GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT	2220
698	T I S R A F M N G S S V E H V V E F G L	717

Figure 6B

2221	TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCGGACAC	2280
718	D Y P E G M A V D W M G K N L Y W A D T	737
2281	TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG	2340
738	G T N R I E V A R L D G Q F R Q V L V W	757
2341	GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG	2400
758	R D L D N P R S L A L D P T K G Y I Y W	777
2401	GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT	2460
778	T E W G G K P R I V R A F M D G T N C M	797
2461	GACGCTGGTGGACAAGGTGGGCGGGCCAAACGACCTCACCATTGACTACGCTGACCAGCG	2520
798	T L V D K V G R A N D L T I D Y A D Q R	817
2521	CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTGAGGA	2580
818	L Y W T D L D T N M I E S S N M L G Q E	837
2581	GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCCGTCTGACGCAGTACAGCGATTA	2640
838	R V V I A D D L P H P F G L T Q Y S D Y	857
2641	TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG	2700
858	I Y W T D W N L H S I E R A D K T S G R	877
2701	GAACCGCACCCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTCTC	2760
878	N R T L I Q G H L D F V M D I L V F H S	897
2761	CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG	2820
898	S R Q D G L N D C M H N N G Q C G Q L C	917
2821	CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCG	2880
918	L A I P G G H R C G C A S H Y T L D P S	937
2881	CAGCCGCAACTGCAGCCCCGCCACACCTTCTTGCTGTTTCAGCCAGAAATCTGCCATCAG	2940
938	S R N C S P P T T F L L F S Q K S A I S	957
2941	TCGGATGATCCCGGACGACGACGACGACCCGGATCTCATCCTGCCCTGCATGGACTGAG	3000
958	R M I P D D Q H S P D L I L P L H G L R	977
3001	GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG	3060
978	N V K A I D Y D P L D K F I Y W V D G R	997
3061	CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG	3120
998	Q N I K R A K D D G T Q P F V L T S L S	1017
3121	CCAAGGCCAAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC	3180
1018	Q G Q N P D R Q P H D L S I D I Y S R T	1037
3181	ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC	3240
1038	L F W T C E A T N T I N V H R L S G E A	1057
3241	CATGGGGGTGGTGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCTCAACGCGGA	3300
1058	M G V V L R G D R D K P R A I V V N A E	1077

Figure 6C

009578900-052500

3301	GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC	3360
1078	R G Y L Y F T N M Q D R A A K I E R A A	1097
3361	CCTGGACGGCACCAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT	3420
1098	L D G T E R E V L F T T G L I R P V A L	1117
3421	GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA	3480
1118	V V D N T L G K L F W V D A D L K R I E	1137
3481	GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC	3540
1138	S C D L S G A N R L T L E D A N I V Q P	1157
3541	TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT	3600
1158	L G L T I L G K H L Y W I D R Q Q Q M I	1177
3601	CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTGCCCCA	3660
1178	E R V E K T T G D K R T R I Q G R V A H	1197
3661	CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCCACCCATG	3720
1198	L T G I H A V E E V S L E E F S A H P C	1217
3721	TGCCCCGTGACAATGGTGGCTGCTCCACATCTGTATTGCCAAGGGTGATGGGACACCACG	3780
1218	A R D N G G C S H I C I A K G D G T P R	1237
3781	GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC	3840
1238	C S C P V H L V L L Q N L L T C G E P P	1257
3841	CACCTGCTCCCCGGACCAAGTTGTCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC	3900
1258	T C S S P D Q F A C A T G E I D C I P G A	1277
3901	CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCGCT	3960
1278	W R C D G F P E C D D Q S D E E G C P V	1297
3961	GTGCTCCGCCGCCAGTTCCCTGCGCGCGGGGTCAAGTGTGTGGACCTGCGCCTGCGCTG	4020
1298	C S A A Q F P C A R G Q C V D L R L R C	1317
4021	CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT	4080
1318	D G E A D C Q D R S D E V D C D A I C L	1337
4081	GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCTCATCAAACAGCAGTGCAGCTC	4140
1338	P N Q F R C A S G Q C V L I K Q Q C D S	1357
4141	CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC	4200
1358	F P D C I D G S D E L M C E I T K P P S	1377
4201	AGACGACAGCCCCGGCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT	4260
1378	D D S P A H S S A I G P V I G I I L S L	1397
4261	CTTCGTATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG	4320
1398	F V M G G V Y F V C Q R V V C Q R Y A G	1417
4321	GGCCAACGGGCCCTTCCCGCACGAGTATGTGACGGGACCCCGCACGTGCCCTCAATTT	4380
1418	A N G P F P H E Y V S G T P H V P L N F	1437

Figure 6D

Northern Blot Analysis - Zmax 1

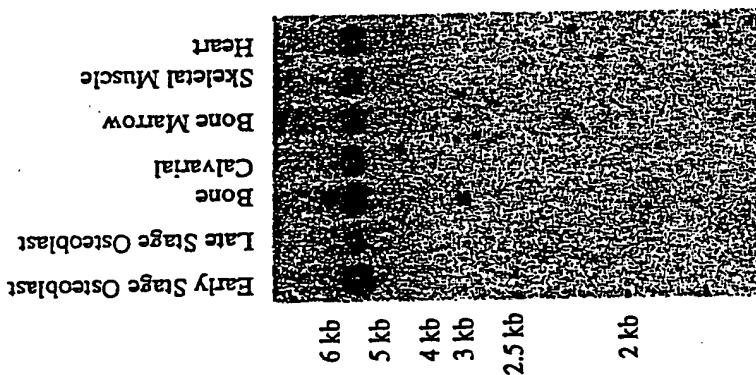


Figure 7B

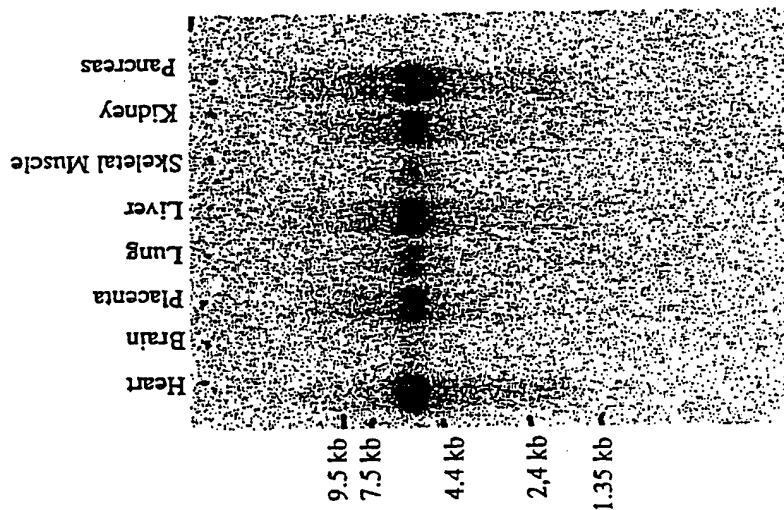
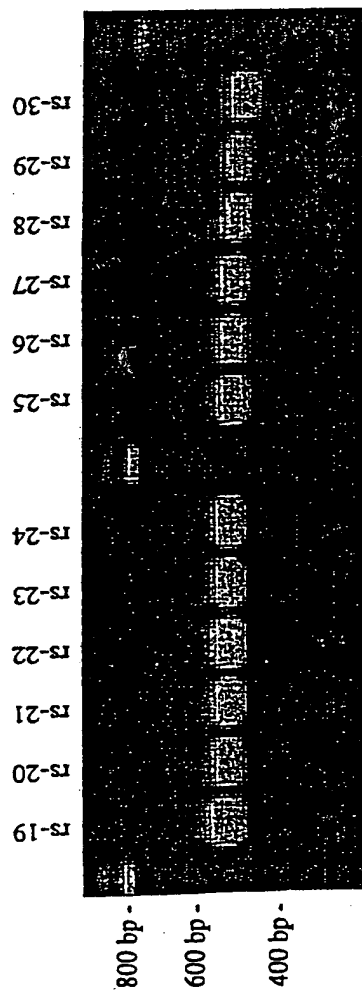


Figure 7A

Z_{\max} 1 random samples

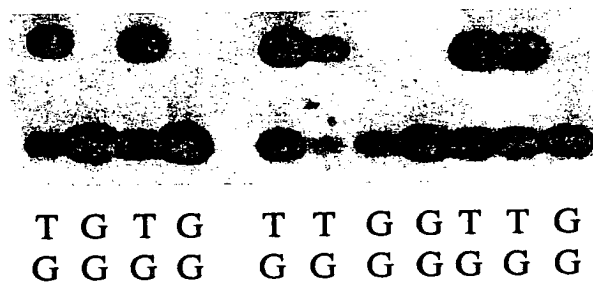
b527d12-h_Contig087C_1.nt

[illegible]

[illegible]

2326 zmax1.ASO.g

Affected
Unaffected
Affected
Unaffected
Affected
Affected
Unaffected
Unaffected
Affected
Affected
Unaffected



Genotype

FIG. 9

Mouse Zmax1 In situ hybridization
100X Magnification

Antisense probe



Sense probe

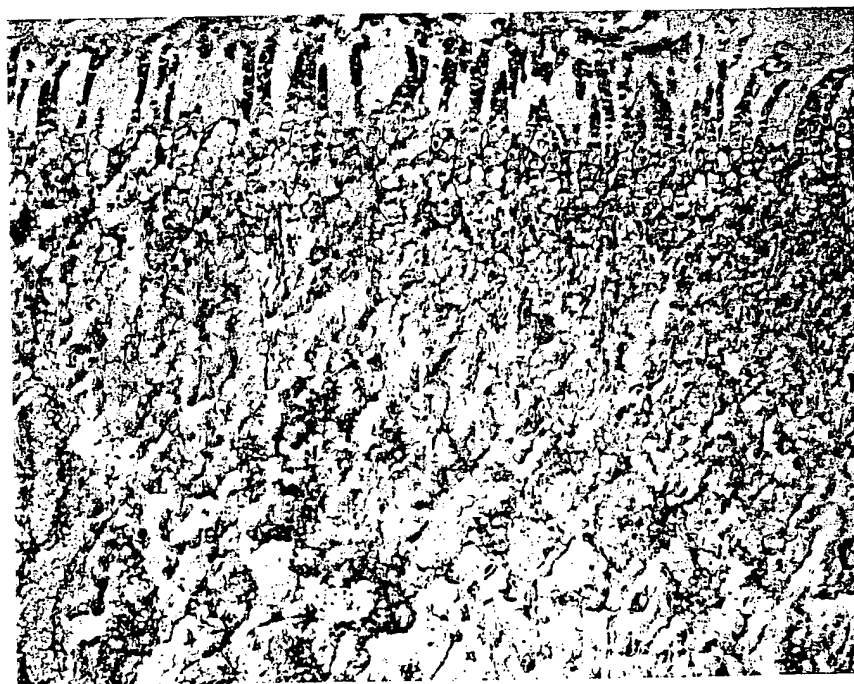


FIG. 10

00578900 052600 009250 00682560

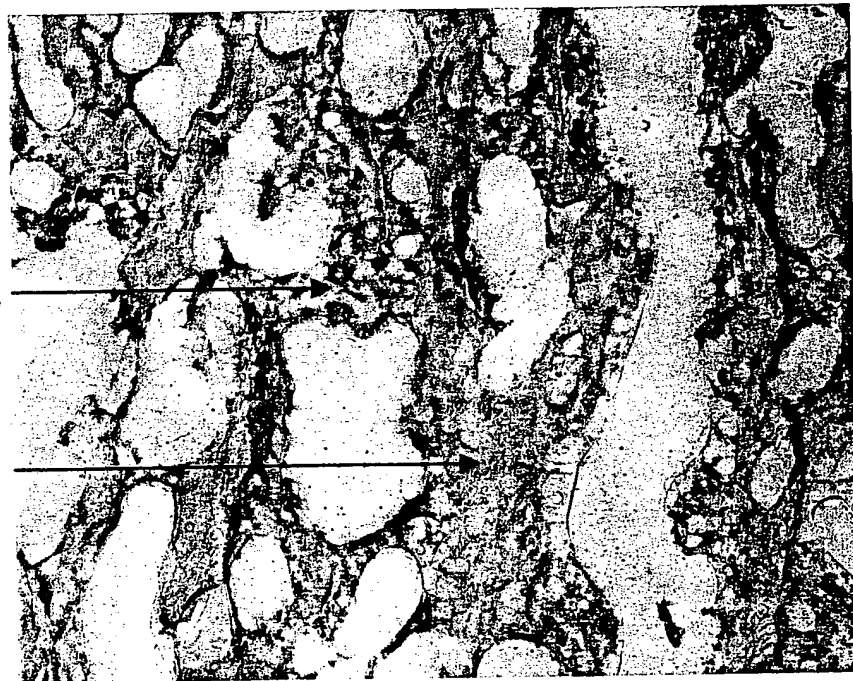
Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts
and osteoclasts

Trabecular
bone

Proximal
Metaphysis



Sense probe



FIG. 11

009250" 00682560

Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts

Endosteum



Sense probe

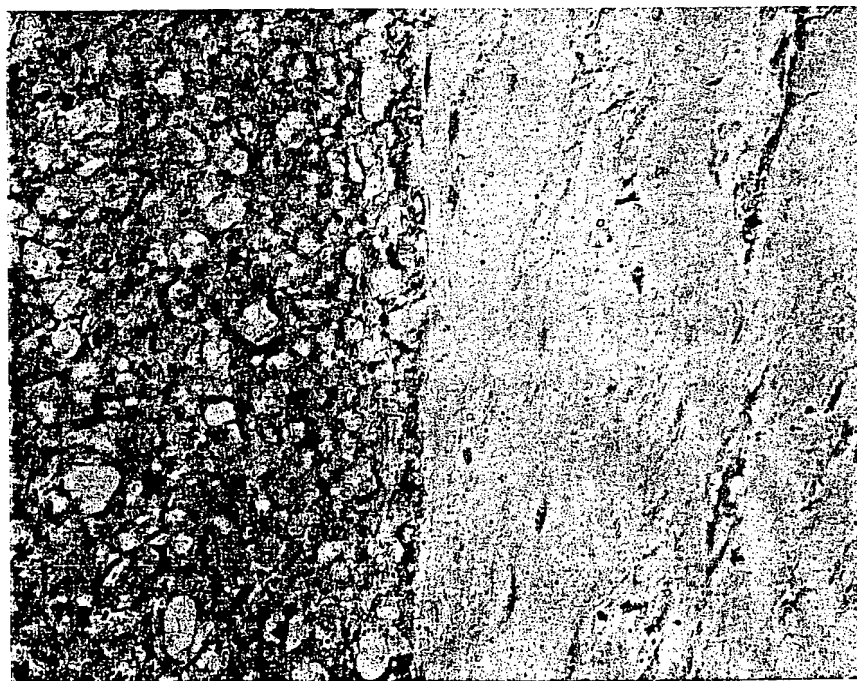


FIG. 12

009250-00684560

Antisense Inhibition of Zmax1 Expression

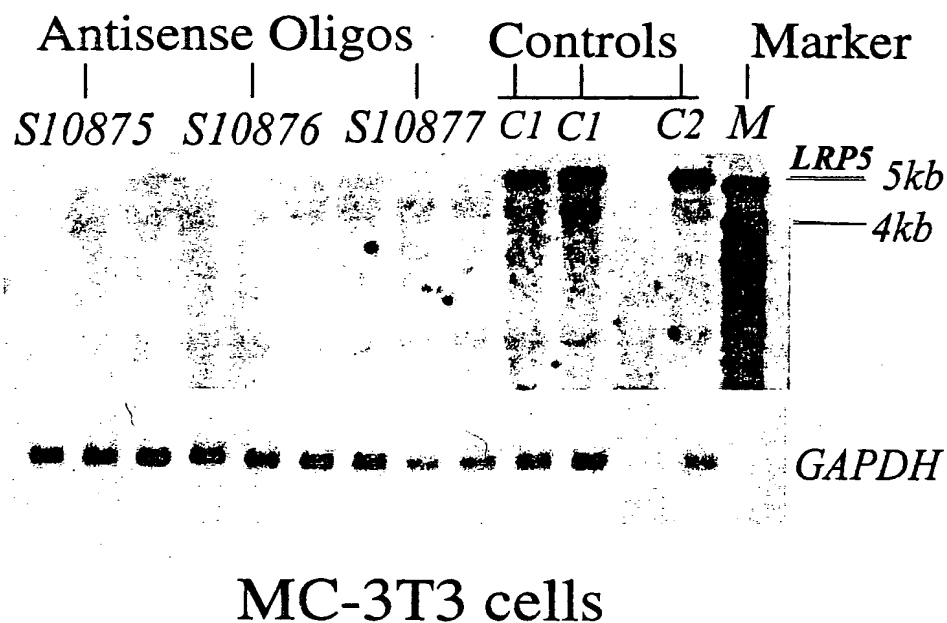


FIG. 13